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From: Seharaseyon, Jegatheesan
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J. Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
Fax: (571)-273-0892

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Searcher: _____
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Searcher Prep/Rev. Time: _____
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Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
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QUESTEL/ORBIT: _____
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SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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LOCUS AX477555 140 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 7 from Patent WO246433.
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VERSION AX477555.1 GI:22216735
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITLE Tnf-inducible promoters and methods for using
JOURNAL Patent: WO 0246433-A 7 13-JUN-2002;
Saus, Juan (ES)
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Db 20 GAGGGTAAATAGTGGGCCAG 1
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DEFINITION Sequence 6 from Patent WO246378.
ACCESSION AX504974
VERSION AX504974.1 GI:23386296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITLE Alternative pol k nucleotide and amino acid sequence and methods
JOURNAL Patent: WO 0246378-A 6 13-JUN-2002;
Saus, Juan (ES)
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DEFINITION Sequence 7 from Patent WO246378.
ACCESSION AX504975
VERSION AX504975.1 GI:23386297
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITLE Alternative pol k nucleotide and amino acid sequence and methods
JOURNAL Patent: WO 0246378-A 7 13-JUN-2002;
Saus, Juan (ES)
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DEFINITION Sequence 4 from Patent WO246433.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITLE Tnf-inducible promoters and methods for using
JOURNAL Patent: WO 0246433-A 4 13-JUN-2002;
Saus, Juan (ES)
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DEFINITION Sequence 7 from Patent WO246378.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITLE Alternative pol k nucleotide and amino acid sequence and methods
JOURNAL Patent: WO 0246378-A 7 13-JUN-2002;
Saus, Juan (ES)
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LOCUS AX477552 771 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 4 from Patent WO246433.
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VERSION AX477552.1 GI:22216732
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITLE Tnf-inducible promoters and methods for using
JOURNAL Patent: WO 0246433-A 4 13-JUN-2002;
Saus, Juan (ES)
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Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX477553 771 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 5 from Patent WO0246378.
ACCESSION AX477553
VERSION AX477553.1 GI:22216733
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITL Trf-inducible promoters and methods for using
JOURNAL Patent: WO 0246378-A 5 13-JUN-2002;
Saus, Juan (ES)
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ACCESSION AX504972
VERSION AX504972.1 GI:23386294
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITL Alternative pol k nucleotide and amino acid sequence and methods
for using
JOURNAL Patent: WO 0246378-A 4 13-JUN-2002;
Saus, Juan (ES)
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ACCESSION AX477551
VERSION AX477551.1 GI:22216731
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITL Alternative pol k nucleotide and amino acid sequence and methods
for using
JOURNAL Patent: WO 0246378-A 5 13-JUN-2002;
Saus, Juan (ES)
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ACCESSION AX477551
VERSION AX477551.1 GI:22216731
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITL Alternative pol k nucleotide and amino acid sequence and methods
for using
JOURNAL Patent: WO 0246378-A 4 13-JUN-2002;
Saus, Juan (ES)
FEATURES
Location/Qualifiers
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Qy 121 GAGGGTAAATAGTGGGCCAG 140
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RESULT 8
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VERSION AX504973.1 GI:23386295
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Saus, J.
TITL Alternative pol k nucleotide and amino acid sequence and methods
for using
JOURNAL Patent: WO 0246378-A 5 13-JUN-2002;
Saus, Juan (ES)
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ACCESSION AX477551
VERSION AX477551.1 GI:22216731
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REFERENCE 1
AUTHORS Saus, J.
TITL Alternative pol k nucleotide and amino acid sequence and methods
for using
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Saus, J.
Tnf-inducible promoters and methods for using

JOURNAL Patent: WO 0246433-A 3 13-JUN-2002;
Saus, Juan (ES)

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AX504971

LOCUS AX504971 955 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 3 from Patent WO0246378.

ACCESSION AX504971

VERSION AX504971.1 GI:23386293

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Saus, J.

Alternative pol k nucleotide and amino acid sequence and methods

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JOURNAL Patent: WO 0246378-A 3 13-JUN-2002;

Saus, Juan (ES)

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QY 121 GAGGGTAAATAGTGGGCCAG 140

Db 846 GAGGGTAAATAGTGGGCCAG 865

RESULT 11

AF315603

LOCUS AF315603 955 bp DNA linear PRI 20-SEP-2002
DEFINITION Homo sapiens DNA polymerase kappa (POLK) and Goodpasture
autoantigen binding protein (COL4A3BP) genes, bidirectional
promoter and partial sequence.

ACCESSION AF315603

VERSION AF315603.1 GI:23208517

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 955)
Granero, F., Revert, F., Raya, A. and Saus, J.

A bidirectional promoter for the genes encoding DNA polymerase
kappa and Goodpasture autoantigen binding protein: Identification
of a novel pol kappa alternative spliced variant

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 955)

Granero, F., Revert, F., Raya, A. and Saus, J.

Direct Submission Patologia Molecular, Fundacion Valenciana
Submitted (23-OCT-2000)

JOURNAL de Investigaciones Biomedicas, Amadeo de Saboya, 4, Valencia,
Valencia 46010, Spain

FEATURES Location/Qualifiers

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ORIGIN /product="Goodpasture autoantigen binding protein"

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QY 121 GAGGGTAAATAGTGGGCCAG 140

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RESULT 12

AC116341/c

LOCUS AC116341

DEFINITION Homo sapiens chromosome 5 clone RP11-144A5, complete sequence.

ACCESSION AC116341

VERSION AC116341.2 GI:21956545

KEYWORDS HTG.

Direct Submission
 TITLE
 JOURNAL
 Submitted (13-JAN-2000) Tomoo Ogi, Institute for Virus Research,
 Kyoto university, Laboratory of Genetic Information Analysis;
 Kawahara-machi, Syogoin, Sakyo-ku, Kyoto, Kyoto 606-8507, Japan
 (E-mail: togi@virus.kyoto-u.ac.jp, Tel:81-75-751-4033(ex.4033),
 Fax:81-75-751-3989)
 FEATURES
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 QY 121 GAGGGTAAATAGTGGGCCAG 140
 Db 3609 GAGGGTAAATAGTGGGCCAG 3590
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 AY273797/c
 LOCUS
 DEFINITION
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 cds.
 AY273797
 AY273797.1 GI:30039654
 .
 Homo sapiens (human)
 Homo sapiens
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 90905)
 Rieder,M.J., Livingston,R.J., Daniels,M.R., Montoya,M.A.,
 Chung,M.-W., Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L.,

TITLE	Robertson,P.D., Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.
JOURNAL	Direct Submission Submitted (09-APR-2003) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT	To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).
FEATURES	Location/Qualifiers
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Db 1984 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTCTCGCTCAGACGCCGCGGAGGGGACG 1925
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|
QY 61 GGGCGGGAGTGTAGTGGGGGAGAAATGGGAGGACGAAGGGGAGGGGAAAGGACAGGGGAGGG 120
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Db 1924 GGGCGGGAGTGTAGTGGGGGAGAAATGGGAGGACGAAGGGGAGGGGAAAGGACAGGGGAGGG 1865
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QY 121 GAGGTAATAATAGTGGGCCAG 140
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|
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RESULT 15
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LOCUS      AC150438      220823 bp      DNA      linear      HTG 20-JUL-2004
DEFINITION Saimiri sciureus clone CH254-237A18, WORKING DRAFT SEQUENCE, 2
ordered pieces.
ACCESSION  AC150438
VERSION    AC150438.1 GI:50399918
KEYWORDS   HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE     Saimiri sciureus (common squirrel monkey)
ORGANISM   Saimiri sciureus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae;
            Saimiri.
REFERENCE  1 (bases 1 to 220823)

```

AUTHORS TITLE REFERENCE AUTHORS TITLE JOURNAL COMMENT

Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
 Peng,Z., Malinov,I. and Rubin,E.M.
 Direct Submission
 Unpublished
 2 (bases 1 to 220823)
 Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
 Peng,Z., Malinov,I. and Rubin,E.M.
 Direct Submission
 Submitted (20-JUL-2004) Genome Sciences, Lawrence Berkeley National
 Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA

Sequence Produced by Berkeley PGA
 Web site: <http://pga.lbl.gov>
 Center Code: PGABERK
 Center Project Name: S070
 Bac Clone Name: CH254-237A18

This sequence has been compared to sequences of other species
 using Vista (<http://www-gsd.lbl.gov/VISTA>). The results can be
 viewed at:
http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=HMGR

The order-orientation of the draft sequence was accomplished by
 using:
 Avid (<http://baboon.math.berkeley.edu/avid>),
 Lagan (<http://lagan.stanford.edu/>) and paired end information.

Funding agent: Programs for Genomic Applications (NHLBI)

Summary Statistics:

Sequencing vector: Plasmid; pUC18
 Chemistry: Dye-terminator Big Dye
 Assembly Program: Phrap version 0.990329.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

* 1 102039: contig of 102039 bp in length
 * 102040 102139: gap of unknown length
 * 102140 220823: contig of 118684 bp in length.

FEATURES

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 /mol_type="genomic DNA"
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ORIGIN

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 Db 199383 GGGCGGGAGTAG-GAGGAGAAATGGGAGGACGAAGGGGAGGGGAAAGGACAGGGGAGGG 199325
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 QY 121 GAGGTAATAATAGTGGGCCAG 140
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 Job time : 1439 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 18:45:18 ; Search time 279 Seconds
(without alignments)
2970.480 Million cell updates/sec

Title: US-10-008-721-6
Perfect score: 140
Sequence: 1 ggggtcggaggaggatccc.....gagggtaaatagtgggccag 140

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: , 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s:*
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7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	140	6 AAD41044	Aad41044 Human COL
2	140	100.0	140	6 AAD41044	Abt03866 Human Goo
3	140	100.0	140	6 AAD41044	Abt03865 Human Goo
4	140	100.0	140	9 ACD13469	Accl13469 Human Pol
5	140	100.0	140	9 ACD13468	Accl13468 Human GPB
6	140	100.0	140	9 ADA97871	Ada97871 Human tum
7	140	100.0	140	9 ADA97870	Ada97870 Human tum
8	140	100.0	771	6 AAD41042	Aad41042 Human COL
9	140	100.0	771	6 AAD41042	Abt03863 Human Goo
10	140	100.0	771	6 AAD41042	Abt03864 Human Goo
11	140	100.0	771	9 ACD13467	Accl13467 Human Pol
12	140	100.0	771	9 ACD13466	Accl13466 Human GPB
13	140	100.0	771	9 ADA97869	Ada97869 Human tum
14	140	100.0	771	9 ADA97868	Ada97868 Human tum
15	140	100.0	955	6 AAD41041	Aad41041 Human 955
16	140	100.0	955	6 ACD13465	Accl13465 Human Goo
17	140	100.0	955	9 ACD13465	Accl13465 Human pol
18	140	100.0	955	9 ADA97867	Ada97867 Human tum
19	48	34.3	26390	4 AAK65971	Aak65971 Human imm
20	47.6	34.0	408	13 ACN50226	Acn50226 Cotton no

21	47.2	33.7	1416	8	ABZ20967	Abz20967 Animal te
22	47	33.6	588	13	ACN54596	Acn54596 Cotton an
23	46.6	33.3	406	13	ACN59490	Acn59490 Cotton gy
24	46.6	33.3	20345	10	ADC86252	Adc86252 Human GPC
25	46.2	33.0	92219	13	ABD33359	Abd33359 Murine ca
26	45.6	32.6	629	13	ACN54594	Acn54594 Cotton an
27	45.2	32.3	1065	6	ABT09682	Abt09682 Human PAL
28	45	32.1	263	13	ACN61884	Acn61884 Cotton gy
29	45	32.1	1385	6	ABQ70117	Abq70117 Listeria
30	45	32.1	1385	6	ABQ68566	Abq68566 Listeria
31	45	32.1	23643	12	ADQ97331_5	Continuation (6 of
32	44.8	32.0	447	13	ACN55700	Acn55700 Cotton an
33	44.6	31.9	3952	4	AAL03258	Aal03258 Human rep
34	44.6	31.9	3955	4	AAL03257	Aal03257 Human rep
35	44.6	31.9	13591	5	AAF80047	Aaf80047 Nucleotid
36	44.4	31.7	31857	10	ADC86230	Adc86230 Human GPC
37	44.4	31.7	11750	13	ABD32653	Abd32653 Human can
38	44.2	31.6	2188	2	AZ77506	Aaz77506 Human ova
39	44.2	31.6	3163	10	ADC87060	Adc87060 Human GPC
40	44	31.4	500	6	ABN15750	Abn15750 Human gen
41	44	31.4	500	13	ACN78840	Acn78840 Human GDM
42	43.8	31.3	987	6	ABT09669	Abt09669 Human PAL
43	43.4	31.0	410	4	AAI82055	Aai82055 Human pol
44	43.4	31.0	566	13	ACN59482	Acn59482 Cotton gy
45	43.4	31.0	600	6	ABQ52497	Abq52497 Oligonuc

ALIGNMENTS

RESULT 1
AAD41044
ID AAD41044 standard; DNA; 140 BP.
XX
AC AAD41044;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human COL4A3BP DNA fragment.
XX
KW Human; tumour necrosis-factor; TNF; promoter; autoimmune disorder;
KW cancer; therapy; db.
XX
OS Homo sapiens.
XX
PN WO200246433-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-EP014412.
XX
PR 08-DEC-2000; 2000US-0254649P.
XX
PA (SAUS/) SAUS J.
XX
PI Saus J;
XX
DR WPI; 2002-519670/55.
XX
PT Novel tumor necrosis-factor inducible promoter useful for identifying
candidate compounds for treating/preventing autoimmune disorders/cancer,
or for identifying promoters that are regulated by tumor necrosis factor.
PS Claim 1; Page 68; 95pp; English.
XX
CC The invention relates to a tumour necrosis-factor TNF inducible promoter.
CC The invention is useful for identifying candidate TNF inducible promoters
CC by aligning a test sequence consisting of a nucleic acid sequence with a
CC comparison sequence selected from the invention, using a gap opening
CC penalty of 50 and a gap extension penalty of 3 to define a test
CC alignment, shuffling the nucleic sequence of the test sequence at least
CC one hundred times, while maintaining its length and composition, to
CC produce a series of randomised sequences, aligning the randomised

CC sequences with the comparison sequence using a gap opening penalty of 50
 CC and a gap extension penalty of 3, to produce a series of randomised
 CC alignments, determining an average alignment quality of the randomised
 CC alignments, where the average alignment quality of the randomised
 CC alignments represent an alignment expected by chance, comparing the test
 CC alignment with the average alignment quality of the randomised alignments
 CC and identifying a test alignment with a probability value of less than
 CC 0.05 that the alignment is obtained by chance as a candidate TNF
 CC inducible promoter. The invention is useful for identifying candidate
 CC compounds for treating or preventing autoimmune disorders or cancer. The
 CC present sequence is human COL4A3BP DNA fragment
 XX
 SQ Sequence 140 BP; 31 A; 19 C; 77 G; 13 T; 0 U; 0 Other;

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 Best Local Similarity 100.0%; Pred. No. 6.6e-24;
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 DB 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGAGGGGACG 60
 QY 61 GGGCGGGAGTACTGGGGGAGATGGAGACCAAGGGAGGGGAAAGGACACGGGGAGGG 120
 DB 61 GGGCGGGAGTACTGGGGGAGATGGAGACCAAGGGAGGGGAAAGGACACGGGGAGGG 120
 QY 121 GAGGGTAAATAGTGGGCCAG 140
 DB 121 GAGGGTAAATAGTGGGCCAG 140

RESULT 2
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 ID ABT03866 standard; DNA; 140 BP.
 XX
 AC ABT03866;
 XX
 DT 18-SEP-2002 (first entry)
 XX
 DE Human Goodpasture antigen binding protein gene fragment #7.
 XX
 KW Human; pol kappa 76; Goodpasture antigen binding protein; GPBP;
 KW* chromosome 5q12-13; apoptosis; autoimmune disorder; cancer; cytostatic;
 KW immunosuppressive; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200246378-A2.
 XX
 PD 13-JUN-2002.

PF 07-DEC-2001; 2001WO-EP014409.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 DR WPI; 2002-537563/57.
 XX
 PT Novel isolated pol kappa76 polypeptide, a 76 kDa alternatively spliced
 PT variant of DNA polymerase kappa useful as target for treating a patient
 PT with autoimmune disorder or cancer.
 XX
 PS Example; Page 63; 90pp; English.

CC The present invention provides the protein and coding sequences of human
 CC DNA polymerase pol kappa 76. The gene is found on human chromosome 5q12-
 CC 13, in a head-to-head arrangement with the Goodpasture antigen binding
 CC protein (GPBP). The detection of the coding sequence can be used for
 CC diagnosing an autoimmune condition and identifying cells undergoing
 CC apoptosis, and the sequences can be used in the treatment of autoimmune

CC diseases and cancer. The present sequence is a gene sequence described in
 CC the invention
 XX
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 DB 140 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGAGGGGACG 81
 QY 61 GGGCGGGAGTACTGGGGGAGATGGAGACCAAGGGAGGGGAAAGGACACGGGGAGGG 120
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 QY 121 GAGGGTAAATAGTGGGCCAG 140
 DB 20 GAGGGTAAATAGTGGGCCAG 1

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 AC ABT03865;
 XX
 DT 18-SEP-2002 (first entry)
 XX
 DE Human Goodpasture antigen binding protein gene fragment #6.
 XX
 KW Human; pol kappa 76; Goodpasture antigen binding protein; GPBP;
 KW* chromosome 5q12-13; apoptosis; autoimmune disorder; cancer; cytostatic;
 KW immunosuppressive; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200246378-A2.
 XX
 PD 13-JUN-2002.

PF 07-DEC-2001; 2001WO-EP014409.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 DR WPI; 2002-537563/57.
 XX
 PT Novel isolated pol kappa76 polypeptide, a 76 kDa alternatively spliced
 PT variant of DNA polymerase kappa, useful as target for treating a patient
 PT with autoimmune disorder or cancer.
 XX
 PS Example; Page 63; 90pp; English.

CC The present invention provides the protein and coding sequences of human.
 CC DNA polymerase pol kappa 76. The gene is found on human chromosome 5q12-
 CC 13, in a head-to-head arrangement with the Goodpasture antigen binding
 CC protein (GPBP). The detection of the coding sequence can be used for
 CC diagnosing an autoimmune condition and identifying cells undergoing
 CC apoptosis, and the sequences can be used in the treatment of autoimmune
 CC diseases and cancer. The present sequence is a gene sequence described in
 CC the invention
 XX

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 Db 1 GGGTTCGGAGGAGGATCCCGAAGGCTCGCGTCTCGCTCAGACGCCGGAGGGGACG 60
 Qy 61 GGGCGGGGAGTGTGGGGGAGAAATGGGAGGACGAAGGAGGGGAAAGGACAGGGGGAGG 120
 Db 61 GGGCGGGGAGTGTGTGGGGGAGAAATGGGAGGACGAAGGAGGGGAAAGGACAGGGGGAGG 120
 Qy 121 GAGGTTAAATAGTGGGCCAG 140
 Db 121 GAGGTTAAATAGTGGGCCAG 140
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 ID ACD13469 standard; DNA; 140 BP.
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 AC ACD13469;
 XX
 DT 14-AUG-2003 (first entry)
 DE Human Pol kappa 76 intergene region/transcription start.
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 KW Human; ds; Goodpasture antigen binding protein; GPBP; COL4A3BP;
 KW collagen 4 alpha 3 binding protein; DNA polymerase kappa; Pol kappa;
 KW Goodpasture disease; cutaneous lupus; polk76; bi-directional promoter;
 KW autoimmune disease; cancer; antisense therapy; chromosome 5q12-13.
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 OS Homo sapiens.
 XX
 PN US2003027165-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 07-DEC-2001; 2001US-00010920.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 XX WPI; 2003-479531/45.
 XX
 XX New isolated DNA polymerase, pol kappa 76, useful in identifying
 PT autoimmune disorders and in treating cancer and autoimmune disorders by
 PT modifying its expression.
 XX
 PS Example; Page 21; 54pp; English.
 XX
 CC The invention relates to an isolated pol kappa (k) 76 polypeptide (an
 CC alternatively spliced form of DNA polymerase kappa), appearing as
 CC ABO07327 (encoded by the cDNA appearing as ACD13492). The gene for
 CC POLKappa is located on chromosome 5q12-13 in a head-head arrangement with
 CC the gene encoding Goodpasture antigen binding protein (GPBP or collagen 4
 CC alpha 3 binding protein (COL4A3BP), associated with autoimmune diseases
 CC such as Goodpasture's disease and cutaneous lupus) i.e. has a bi-
 CC directional promoter. Also included are a recombinant expression vector
 CC comprising the polk76 cDNA, a host cell transfected with the vector,
 CC detecting (M1) polk76 (comprising providing a protein sample to be
 CC screened, contacting the protein sample to be screened with an anti-
 CC polk76 antibody and detecting the formation of an antibody-polypeptide
 CC complexes, where the presence of the antibody-polypeptide complexes
 CC indicates the presence of polk76), detecting (M2) the polk76 nucleic acid
 CC in a sample (comprising contacting the sample with one or more polk76 PCR
 CC primer, carrying out PCR to generate PCR products, and identifying the
 CC polk76-specific PCR), detecting an autoimmune condition in a patient
 CC (comprising providing a tissue or body fluid sample from the patient,
 CC providing a control tissue or body fluid sample in which no autoimmune
 CC condition is present, and detecting an increase in pol k76 RNA expression
 CC in the tissue of body fluid samples compared to the control sample, where
 CC the increase indicates the presence of an autoimmune condition) and
 CC treating (M3) a patient with an autoimmune disorder or cancer by

CC modifying the expression or activity of pol k76 in the patient. Modifying
 CC the expression or activity of polk76 or polk76 nucleic acid, such as by
 CC increasing or decreasing their expression or activity using antibodies or
 CC antisense therapy, is useful for treating an autoimmune disorder or
 CC cancer. The present sequence is a PCR fragment representing part (or all)
 CC of the intergenic region or bi-directional promoter of the polkappa/GPBP
 CC genes
 XX
 SQ Sequence 140 BP; 13 A; 77 C; 19 G; 31 T; 0 U; 0 Other;
 Query Match 100.0%; Score 140; DB 9; Length 140;
 Best Local Similarity 100.0%; Pred. No. 6.e-24;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGGTTCGGAGGAGGATCCCGAAGGCTCGCGTCTCGCTCAGACGCCGGAGGGGACG 60
 Db 140 GGGTTCGGAGGAGGATCCCGAAGGCTCGCGTCTCGCTCAGACGCCGGAGGGGACG 81
 Qy 61 GGGCGGGGAGTGTGGGGGAGAAATGGGAGGACGAAGGAGGGGAAAGGACAGGGGGAGG 120
 Db 80 GGGCGGGGAGTGTGTGGGGGAGAAATGGGAGGACGAAGGAGGGGAAAGGACAGGGGGAGG 21
 Qy 121 GAGGTTAAATAGTGGGCCAG 140
 Db 20 GAGGTTAAATAGTGGGCCAG 1
 RESULT 5
 ACD13468
 ID ACD13468 standard; DNA; 140 BP.
 XX
 AC ACD13468;
 XX
 DT 14-AUG-2003 (first entry)
 DE Human GPBP/COL4A3BP intergene region/transcription start.
 XX
 KW Human; ds; Goodpasture antigen binding protein; GPBP; COL4A3BP;
 KW collagen 4 alpha 3 binding protein; DNA polymerase kappa; Pol kappa;
 KW Goodpasture disease; cutaneous lupus; polk76; bi-directional promoter;
 KW autoimmune disease; cancer; antisense therapy; chromosome 5q12-13.
 XX
 OS Homo sapiens.
 XX
 PN US2003027165-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 07-DEC-2001; 2001US-00010920.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 XX WPI; 2003-479531/45.
 XX
 PT New isolated DNA polymerase, pol kappa 76, useful in identifying
 PT autoimmune disorders and in treating cancer and autoimmune disorders by
 PT modifying its expression.
 XX
 PS Example; Page 21; 54pp; English.
 XX
 CC The invention relates to an isolated pol kappa (k) 76 polypeptide (an
 CC alternatively spliced form of DNA polymerase kappa), appearing as
 CC ABO07327 (encoded by the cDNA appearing as ACD13492). The gene for
 CC POLKappa is located on chromosome 5q12-13 in a head-head arrangement with
 CC the gene encoding Goodpasture antigen binding protein (GPBP or collagen 4
 CC alpha 3 binding protein (COL4A3BP), associated with autoimmune diseases
 CC such as Goodpasture's disease and cutaneous lupus) i.e. has a bi-
 CC directional promoter. Also included are a recombinant expression vector
 CC comprising the polk76 cDNA, a host cell transfected with the vector,
 CC detecting (M1) polk76 (comprising providing a protein sample to be
 CC screened, contacting the protein sample to be screened with an anti-
 CC polk76 antibody and detecting the formation of an antibody-polypeptide
 CC complexes, where the presence of the antibody-polypeptide complexes
 CC indicates the presence of polk76), detecting (M2) the polk76 nucleic acid
 CC in a sample (comprising contacting the sample with one or more polk76 PCR
 CC primer, carrying out PCR to generate PCR products, and identifying the
 CC polk76-specific PCR), detecting an autoimmune condition in a patient
 CC (comprising providing a tissue or body fluid sample from the patient,
 CC providing a control tissue or body fluid sample in which no autoimmune
 CC condition is present, and detecting an increase in pol k76 RNA expression
 CC in the tissue of body fluid samples compared to the control sample, where
 CC the increase indicates the presence of an autoimmune condition) and
 CC treating (M3) a patient with an autoimmune disorder or cancer by

CC detecting (M1) polk76 (comprising providing a protein sample to be
 CC screened, contacting the protein sample to be screened with an anti-
 CC polk76 antibody and detecting the formation of an antibody- polypeptide
 CC complexes, where the presence of the antibody-polypeptide complexes
 CC indicates the presence of polk76), detecting (M2) the polk76 nucleic acid
 CC in a sample (comprising contacting the sample with one or more polk76 PCR
 CC primer, carrying out PCR to generate PCR products, and identifying the
 CC polk76-specific PCR), detecting an autoimmune condition in a patient
 CC (comprising providing a tissue or body fluid sample from the patient,
 CC providing a control tissue or body fluid sample in which no autoimmune
 CC condition is present, and detecting an increase in pol k76 RNA expression
 CC in the tissue of body fluid samples compared to the control sample, where
 CC the increase indicates the presence of an autoimmune condition) and
 CC treating (M3) a patient with an autoimmune disorder or cancer by
 CC modifying the expression or activity of pol k76 in the patient. Modifying
 CC the expression or activity of polk76 or polk76 nucleic acid, such as by
 CC increasing or decreasing their expression or activity using antibodies or
 CC antisense therapy, is useful for treating an autoimmune disorder or
 CC cancer. The present sequence is a PCR fragment representing part (or all)
 CC of the intergenic region or bi-directional promoter of the polkappa/GPBP
 CC genes
 XX
 SQ Sequence 140 BP; 31 A; 19 C; 77 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 140; DB 9; Length 140;
 Best Local Similarity 100.0%; Pred. No. 6.6e-24;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGTTCGGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACCGCGGGAGGGGACG 60
 DB 1 GGGTTCGGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACCGCGGGAGGGGACG 60
 QY 61 GGGCGGGGAGTAGTGGGGAGGATGGAGACGAGGAGGGGAGGAGGAGGAGGAGG 120
 DB 61 GGGCGGGGAGTAGTGGGGAGGATGGAGACGAGGAGGGGAGGAGGAGGAGGAGG 120
 QY 121 GAGGGTAAATAGTGGGCCAG 140
 DB 121 GAGGGTAAATAGTGGGCCAG 140

RESULT 6
 ADA97871/c
 ID ADA97871 standard; DNA; 140 BP.
 XX
 AC ADA97871;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human tumour necrosis factor (TNF) inducible promoter #5.
 XX
 KW Human; tumour necrosis factor inducible promoter; TNF;
 KW autoimmune disorder; cancer; ds; promoter; immunosuppressive; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003082745-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 07-DEC-2001; 2001US-00008721.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 DR WPI; 2003-606062/57.

XX New tumor necrosis factor inducible promoters, useful for identifying
 PT promoters that are regulated by tumor necrosis factor, or for identifying
 PT candidate compounds for treating or preventing autoimmune disorders or

PT cancer.
 XX
 XX Claim 1; Fig 1; 57pp; English.
 XX
 CC The invention relates to a tumour necrosis factor (TNF) inducible
 CC promoter. Also disclosed are an expression vector comprising one or more
 CC tumour necrosis factor inducible promoters and a recombinant host cell
 CC transfected with one or more expression vectors. The TNF inducible
 CC promoters, expression vectors and host cells are useful for identifying
 CC promoters that are regulated by tumour necrosis factor or for identifying
 CC candidate compounds for treating or preventing autoimmune disorders or
 CC cancer. This sequence represents a tumour necrosis factor inducible
 CC promoter of the invention.
 XX
 SQ Sequence 140 BP; 13 A; 77 C; 19 G; 31 T; 0 U; 0 Other;
 Query Match 100.0%; Score 140; DB 9; Length 140;
 Best Local Similarity 100.0%; Pred. No. 6.6e-24;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGTTCGGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACCGCGGGAGGGGACG 60
 DB 140 GGGTTCGGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACCGCGGGAGGGGACG 81
 QY 61 GGGCGGGGAGTAGTGGGGAGGATGGAGACGAGGAGGGGAGGAGGAGGAGGAGG 120
 DB 80 GGGCGGGGAGTAGTGGGGAGGATGGAGACGAGGAGGGGAGGAGGAGGAGGAGG 21
 QY 121 GAGGGTAAATAGTGGGCCAG 140
 DB 20 GAGGGTAAATAGTGGGCCAG 1
 RESULT 7
 ADA97870
 ID ADA97870 standard; DNA; 140 BP.
 XX
 AC ADA97870;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human tumour necrosis factor (TNF) inducible promoter #4.
 XX
 KW Human; tumour necrosis factor inducible promoter; TNF;
 KW autoimmune disorder; cancer; ds; promoter; immunosuppressive; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003082745-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 07-DEC-2001; 2001US-00008721.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 DR WPI; 2003-606062/57.
 XX
 PT New tumor necrosis factor inducible promoters, useful for identifying
 PT promoters that are regulated by tumor necrosis factor, or for identifying
 PT candidate compounds for treating or preventing autoimmune disorders or
 PT cancer.
 XX
 XX Claim 1; Fig 1; 57pp; English.
 XX
 CC The invention relates to a tumour necrosis factor (TNF) inducible
 CC promoter. Also disclosed are an expression vector comprising one or more
 CC tumour necrosis factor inducible promoters and a recombinant host cell
 CC transfected with one or more expression vectors. The TNF inducible

CC promoters, expression vectors and host cells are useful for identifying
 CC promoters that are regulated by tumour necrosis factor or for identifying
 CC candidate compounds for treating or preventing autoimmune disorders or
 CC cancer. This sequence represents a tumour necrosis factor inducible
 CC promoter of the invention.

SQ Sequence 140 BP; 31 A; 19 C; 77 G; 13 T; 0 U; 0 Other;
 Query Match 100.0%; Score 140; DB 9; Length 140;
 Best Local Similarity 100.0%; Pred. No. 6.6e-24;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGTTCGGAGGAGGATCCGAGGCTCGCGTGTCCGCTCAGACGCCGGAGGGGAGCG 60
 DB 1 GGGTTCGGAGGAGGATCCGAGGCTCGCGTGTCCGCTCAGACGCCGGAGGGGAGCG 60
 QY 61 GGGCGGGGAGTACGCGGGGAGATGGGAGGACGAGGAGGGGAGGAGGAGGAGG 120
 DB 61 GGGCGGGGAGTACGCGGGGAGATGGGAGGACGAGGAGGGGAGGAGGAGGAGG 120
 QY 121 GAGGGTAAATAGTGGGCCAG 140
 DB 121 GAGGGTAAATAGTGGGCCAG 140

RESULT 8
 AAD41042
 ID AAD41042 standard; DNA; 771 BP.
 AC AAD41042;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human COL4A3BP DNA.
 XX
 XX Human; tumour necrosis-factor; TNF; promoter; autoimmune disorder;
 KW cancer; therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200246433-A2.
 XX
 PD 13-JUN-2002;
 XX
 PF 07-DEC-2001; 2001WO-EP014412.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 DR WPI; 2002-519670/55.
 XX
 XX Novel tumor necrosis-factor inducible promoter useful for identifying
 PT candidate compounds for treating/preventing autoimmune disorders/cancer,
 PT or for identifying promoters that are regulated by tumor necrosis factor.
 XX
 PS Claim 1; Page 67; 95pp; English.
 XX
 XX The invention relates to a tumour necrosis-factor TNF inducible promoter.
 CC The invention is useful for identifying candidate TNF inducible promoters
 CC by aligning a test sequence consisting of a nucleic acid sequence with a
 CC comparison sequence selected from the invention, using a gap opening
 CC penalty of 50 and a gap extension penalty of 3 to define a test
 CC alignment, shuffling the nucleic sequence of the test sequence at least
 CC one hundred times, while maintaining its length and composition, to
 CC produce a series of randomised sequences, aligning the randomised
 CC sequences with the comparison sequence using a gap opening penalty of 50
 CC and a gap extension penalty of 3, to produce a series of randomised
 CC alignments, determining an average alignment quality of the randomised
 CC alignments, where the average alignment quality of the randomised
 CC alignments represent an alignment expected by chance, comparing the test

CC alignment with the average alignment quality of the randomised alignments
 CC and identifying a test alignment with a probability value of less than
 CC 0.05 that the alignment is obtained by chance as a candidate TNF
 CC inducible promoter. The invention is useful for identifying candidate
 CC compounds for treating or preventing autoimmune disorders or cancer. The
 CC present sequence is human COL4A3BP DNA

SQ Sequence 771 BP; 186 A; 209 C; 253 G; 123 T; 0 U; 0 Other;
 Query Match 100.0%; Score 140; DB 6; Length 771;
 Best Local Similarity 100.0%; Pred. No. 6.7e-24;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGTTCGGAGGAGGATCCGAGGCTCGCGTGTCCGCTCAGACGCCGGAGGGGAGCG 60
 DB 577 GGGTTCGGAGGAGGATCCGAGGCTCGCGTGTCCGCTCAGACGCCGGAGGGGAGCG 636
 QY 61 GGGCGGGGAGTACGCGGGGAGATGGGAGGACGAGGAGGGGAGGAGGAGGAGG 120
 DB 637 GGGCGGGGAGTACGCGGGGAGATGGGAGGACGAGGAGGGGAGGAGGAGGAGG 696
 QY 121 GAGGGTAAATAGTGGGCCAG 140
 DB 697 GAGGGTAAATAGTGGGCCAG 716

RESULT 9
 ABT03863
 ID ABT03863 standard; DNA; 771 BP.
 XX
 AC ABT03863;
 XX
 DT 18-SEP-2002 (first entry)
 XX
 DE Human Goodpasture antigen binding protein gene fragment #4.
 XX
 KW Human; pol kappa 76; Goodpasture antigen binding protein; GPBP;
 KW chromosome 5q12-13; apoptosis; autoimmune disorder; cancer; cytostatic;
 KW immunosuppressive; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200246378-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 07-DEC-2001; 2001WO-EP014409.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 DR WPI; 2002-537563/57.
 XX
 XX Novel isolated pol kappa76 polypeptide, a 76 kDa alternatively spliced
 PT variant of DNA polymerase kappa, useful as target for treating a patient
 PT with autoimmune disorder or cancer.
 XX
 PS Example; Page 62; 90pp; English.
 XX
 XX The present invention provides the protein and coding sequences of human
 CC DNA polymerase pol kappa 76. The gene is found on human chromosome 5q12-
 CC 13, in a head-to-head arrangement with the Goodpasture antigen binding
 CC protein (GPBP). The detection of the coding sequence can be used for
 CC diagnosing an autoimmune condition and identifying cells undergoing
 CC apoptosis, and the sequences can be used in the treatment of autoimmune
 CC diseases and cancer. The present sequence is a gene sequence described in
 CC the invention
 XX
 SQ Sequence 771 BP; 186 A; 209 C; 253 G; 123 T; 0 U; 0 Other;

Query Match 100.0%; Score 140; DB 6; Length 771;
 Best Local Similarity 100.0%; Pred. No. 6.7e-24;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTTCGGAGGAGGATCCGAAAGGCTCGCGTGTGCGCTCAGACGCCGGAGGGGAGC 60
 |||||
 Db 577 GCGTTCGGAGGAGGATCCGAAAGGCTCGCGTGTGCGCTCAGACGCCGGAGGGGAGC 636
 |||||

QY 61 GCGCGGGAGTACTGGGGAGATGGGAGCAGGAGGAGGGGAGGACAGGAGGG 120
 |||||
 Db 637 GCGCGGGAGTACTGGGGAGATGGGAGCAGGAGGAGGGGAGGAGGAGGAGGG 696
 |||||

QY 121 GAGGGTAAATAGTGGGCCAG 140
 |||||
 Db 697 GAGGGTAAATAGTGGGCCAG 716
 |||||

RESULT 10
 ABT03864/c
 ID ABT03864 standard; DNA; 771 BP.
 XX
 AC ABT03864;
 XX
 DT 18-SEP-2002 (first entry)
 XX
 DE Human Goodpasture antigen binding protein gene fragment #5.
 XX
 KW Human; pol kappa 76; Goodpasture antigen binding protein; GPBP;
 KW chromosome 5q12-13; apoptosis; autoimmune disorder; cancer; cytostatic;
 KW immunosuppressive; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200246378-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 07-DEC-2001; 2001WO-EP014409.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 DR WPI; 2002-537563/57.
 XX
 PT Novel isolated pol kappa76 polypeptide, a 76 kDa alternatively spliced
 PT variant of DNA polymerase kappa, useful as target for treating a patient
 PT with autoimmune disorder or cancer.
 XX
 PS Example; Page 63; 90pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC DNA polymerase pol kappa 76. The gene is found on human chromosome 5q12-
 CC 13, in a head-to-head arrangement with the Goodpasture antigen binding
 CC protein (GPBP). The detection of the coding sequence can be used for
 CC diagnosing an autoimmune condition and identifying cells undergoing
 CC apoptosis, and the sequences can be used in the treatment of autoimmune
 CC diseases and cancer. The present sequence is a gene sequence described in
 CC the invention
 XX
 SQ Sequence 771 BP; 123 A; 253 C; 209 G; 186 T; 0 U; 0 Other;

Query Match 100.0%; Score 140; DB 6; Length 771;
 Best Local Similarity 100.0%; Pred. No. 6.7e-24;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTTCGGAGGAGGATCCGAAAGGCTCGCGTGTGCGCTCAGACGCCGGAGGGGAGC 60
 |||||
 Db 195 GGGTTCGGAGGAGGAGATCCCGAAAGGCTCGCGTGTGCGCTCAGACGCCGGAGGGGAGC 136
 |||||

QY 61 GCGCGGGAGTACTGGGGAGATGGGAGCAGGAGGAGGGGAGGAGGAGGAGGG 120
 |||||

Db 135 GCGCGGGAGTACTGGGGAGATGGGAGCAGGAGGAGGGGAGGAGGAGGAGG 76
 |||||

QY 121 GAGGGTAAATAGTGGGCCAG 140
 |||||

Db 75 GAGGGTAAATAGTGGGCCAG 56
 |||||

RESULT 11
 ACD13467/c
 ID ACD13467 standard; DNA; 771 BP.
 XX
 AC ACD13467;
 XX
 DT 14-AUG-2003 (first entry)
 XX
 DE Human Pol kappa 76 771bp PCR fragment.
 XX
 KW Human; ds; Goodpasture antigen binding protein; GPBP; COL4A3BP;
 KW collagen 4 alpha 3 binding protein; DNA polymerase kappa; Pol kappa;
 KW Goodpasture disease; cutaneous lupus; polk76; bi-directional promoter;
 KW autoimmune disease; cancer; antisense therapy; chromosome 5q12-13.
 XX
 OS Homo sapiens.
 XX
 PN US2003027165-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 07-DEC-2001; 2001US-00010920.
 XX
 PR 08-DEC-2000; 2000US-0254649P.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 DR WPI; 2003-479531/45.
 XX
 PT New isolated DNA polymerase, pol kappa 76, useful in identifying
 PT autoimmune disorders and in treating cancer and autoimmune disorders by
 PT modifying its expression.
 XX
 PS Example; Page 21; 54pp; English.
 XX
 CC The invention relates to an isolated pol kappa (k) 76 polypeptide (an
 CC alternatively spliced form of DNA polymerase kappa), appearing as
 CC ABO07327 (encoded by the cDNA appearing as ACD13492). The gene for
 CC POLKappa is located on chromosome 5q12-13 in a head-head arrangement with
 CC the gene encoding Goodpasture antigen binding protein (GPBP or collagen 4
 CC alpha 3 binding protein (COL4A3bp)), associated with autoimmune diseases
 CC such as Goodpasture's disease and cutaneous lupus) i.e. has a bi-
 CC directional promoter. Also included are a recombinant expression vector
 CC comprising the polk76 cDNA, a host cell transfected with the vector,
 CC detecting (M1) polk76 (comprising providing a protein sample to be
 CC screened, contacting the protein sample to be screened with an anti-
 CC polk76 antibody and detecting the formation of an antibody- polypeptide
 CC complexes, where the presence of the antibody-polypeptide complexes
 CC indicates the presence of polk76), detecting (M2) the polk76 nucleic acid
 CC in a sample (comprising contacting the sample with one or more polk76 PCR
 CC primer, carrying out PCR to generate PCR products, and identifying the
 CC polk76-specific PCR), detecting an autoimmune condition in a patient
 CC (comprising providing a tissue or body fluid sample from the patient,
 CC providing a control tissue or body fluid sample in which no autoimmune
 CC condition is present, and detecting an increase in pol k76 RNA expression
 CC in the tissue of body fluid samples compared to the control sample, where
 CC the increase indicates the presence of an autoimmune condition) and
 CC treating (M3) a patient with an autoimmune disorder or cancer by
 CC modifying the expression or activity of pol k76 in the patient. Modifying
 CC the expression or activity of polk76 or polk76 nucleic acid, such as by
 CC increasing or decreasing their expression or activity using antibodies or
 CC antisense therapy, is useful for treating an autoimmune disorder or
 CC cancer. The present sequence is a PCR fragment representing part (or all)

CC of the intergenic region or bi-directional promoter of the polkappa/GPBP
CC genes
XX
SQ Sequence 771 BP; 123 A; 253 C; 209 G; 186 T; 0 U; 0 Other;
Query Match 100.0%; Score 140; DB 9; Length 771;
Best Local Similarity 100.0%; Pred. No. 6.7e-24;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGGGAGCG 60
DB 195 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGGGAGCG 136
QY 61 GGGCGGGGAGTAGTGGGGGAGATGGGAGACGAAGGGAGGGGAAAGGACAGGGGAGGG 120
DB 135 GGGCGGGGAGTAGTGGGGGAGATGGGAGGACGAAGGGAGGGGAAAGGACAGGGGAGGG 76
QY 121 GAGGGTAAATAGTGGGCCAG 140
DB 75 GAGGGTAAATAGTGGGCCAG 56
RESULT 12
ACD13466
ID ACD13466 standard; DNA; 771 BP.
XX
AC ACD13466;
XX
DT 14-AUG-2003 (first entry)
XX
XX Human GPBP/COL4A3BP 771bp PCR fragment.
XX
KW Human; ds; Goodpasture antigen binding protein; GPBP; COL4A3BP;
KW collagen 4 alpha 3 binding protein; DNA polymerase kappa; Pol kappa;
KW Goodpasture disease; cutaneous lupus; polk76; bi-directional promoter;
KW autoimmune disease; cancer; antisense therapy; chromosome 5q12-13.
XX
OS Homo sapiens.
XX
XX US2003027165-A1.
XX
XX 06-FEB-2003.
XX
XX 07-DEC-2001; 2001US-00010920.
XX
XX 08-DEC-2000; 2000US-0254649P.
XX
XX (SAUS/) SAUS J.
XX
XX Saus J;
XX
XX WPI; 2003-479531/45.
XX
XX New isolated DNA polymerase, pol kappa 76, useful in identifying
XX autoimmune disorders and in treating cancer and autoimmune disorders by
XX modifying its expression.
XX
XX Example; Page 20-21; 54pp; English.
XX
XX The invention relates to an isolated pol kappa (k) 76 polypeptide (an
XX alternatively spliced form of DNA polymerase kappa), appearing as
XX ABO07327 (encoded by the cDNA appearing as ACD13492). The gene for
XX POLKAPPA is located on chromosome 5q12-13 in a head-head arrangement with
XX the gene encoding Goodpasture antigen binding protein (GPBP or collagen 4
XX alpha 3 binding protein (COL4A3bp), associated with autoimmune diseases
XX such as Goodpasture's disease and cutaneous lupus) i.e. has a bi-
XX directional promoter. Also included are a recombinant expression vector
XX comprising the polk76 cDNA, a host cell transfected with the vector,
XX detecting (M1) polk76 (comprising providing a protein sample to be
XX screened, contacting the protein sample to be screened with an anti-
XX polk76 antibody and detecting the formation of an antibody-polypeptide
XX complexes, where the presence of the antibody-polypeptide complexes
XX indicates the presence of polk76), detecting (M2) the polk76 nucleic acid

CC in a sample (comprising contacting the sample with one or more polk76 PCR
CC primer, carrying out PCR to generate PCR products, and identifying the
CC polk76-specific PCR), detecting an autoimmune condition in a patient
CC (comprising providing a tissue or body fluid sample from the patient,
CC providing a control tissue or body fluid sample in which no autoimmune
CC condition is present, and detecting an increase in pol k76 RNA expression
CC in the tissue of body fluid samples compared to the control sample, where
CC the increase indicates the presence of an autoimmune condition) and
CC treating (M3) a patient with an autoimmune disorder or cancer by
CC modifying the expression or activity of pol k76 in the patient. Modifying
CC the expression or activity of polk76 or polk76 nucleic acid, such as by
CC increasing or decreasing their expression or activity using antibodies or
CC antisense therapy, is useful for treating an autoimmune disorder or
CC cancer. The present sequence is a PCR fragment representing part (or all)
CC of the intergenic region or bi-directional promoter of the polkappa/GPBP
XX genes
SQ Sequence 771 BP; 186 A; 209 C; 253 G; 123 T; 0 U; 0 Other;
Query Match 100.0%; Score 140; DB 9; Length 771;
Best Local Similarity 100.0%; Pred. No. 6.7e-24;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGGGAGCG 60
DB 577 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGGGAGCG 636
QY 61 GGGCGGGGAGTAGTGGGGGAGATGGGAGACGAAGGGAGGGGAAAGGACAGGGGAGGG 120
DB 637 GGGCGGGGAGTAGTGGGGGAGATGGGAGGACGAAGGGAGGGGAAAGGACAGGGGAGGG 696
QY 121 GAGGGTAAATAGTGGGCCAG 140
DB 697 GAGGGTAAATAGTGGGCCAG 716
RESULT 13
ADA97869/c
ID ADA97869 standard; DNA; 771 BP.
XX
XX ADA97869;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human tumour necrosis factor (TNF) inducible promoter #3.
XX
XX Human; tumour necrosis factor inducible promoter; TNF;
XX autoimmune disorder; cancer; ds; promoter; immunosuppressive; cytostatic.
XX
XX Homo sapiens.
XX
XX US2003082745-A1.
XX
XX 01-MAY-2003.
XX
XX 07-DEC-2001; 2001US-00008721.
XX
XX 08-DEC-2000; 2000US-0254649P.
XX
XX (SAUS/) SAUS J.
XX
XX Saus J;
XX
XX WPI; 2003-606062/57.
XX
XX New tumor necrosis factor inducible promoters, useful for identifying
XX promoters that are regulated by tumor necrosis factor, or for identifying
XX candidate compounds for treating or preventing autoimmune disorders or
XX cancer.
XX
XX Claim 1; Fig 1; 57pp; English.
XX
XX The invention relates to a tumour necrosis factor (TNF) inducible

CC promoter. Also disclosed are an expression vector comprising one or more
CC tumour necrosis factor inducible promoters and a recombinant host cell
CC transfected with one or more expression vectors. The TNF inducible
CC promoters, expression vectors and host cells are useful for identifying
CC promoters that are regulated by tumour necrosis factor or for identifying
CC candidate compounds for treating or preventing autoimmune disorders or
CC cancer. This sequence represents a tumour necrosis factor inducible
CC promoter of the invention.

XX SQ Sequence 771 BP; 123 A; 253 C; 209 G; 186 T; 0 U; 0 Other;
Query Match 100.0%; Score 140; DB 9; Length 771;
Best Local Similarity 100.0%; Pred. No. 6.7e-24;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGATCCGGAAGGCTCGCGTGTGTCGCTCAGACCGCGGAGGGGACG 60
DB 195 GGGTTCGGGAGGAGATCCGGAAGGCTCGCGTGTGTCGCTCAGACCGCGGAGGGGACG 136
QY 61 GGGCGGGGAGTAGTGGGGAGATGGAGACGAAGGGGAGGGAAGGACAGGGGAGGG 120
DB 135 GGGCGGGGAGTAGTGGGGAGATGGAGACGAAGGGGAGGGAAGGACAGGGGAGGG 76
QY 121 GAGGGTAAATAGTGGGCCAG 140
DB 75 GAGGGTAAATAGTGGGCCAG 56

RESULT 14
ADA97868
ID ADA97868 standard; DNA; 771 BP.
AC ADA97868;
XX 20-NOV-2003 (first entry)
DE Human tumour necrosis factor (TNF) inducible promoter #2.
XX Human; tumour necrosis factor inducible promoter; TNF;
KW autoimmune disorder; cancer; ds; promoter; immunosuppressive; cytostatic.
XX Homo sapiens.
XX US2003082745-A1.
XX 01-MAY-2003.
XX 07-DEC-2001; 2001US-00008721.
XX 08-DEC-2000; 2000US-0254649P.
XX (SAUS/) SAUS J.
XX Saus J;
XX WPI; 2003-606062/57.
XX New tumor necrosis factor inducible promoters, useful for identifying
PT promoters that are regulated by tumor necrosis factor, or for identifying
PT candidate compounds for treating or preventing autoimmune disorders or
PT cancer.
XX Claim 1; Fig 1; 57pp; English.
XX The invention relates to a tumour necrosis factor (TNF) inducible
CC promoter. Also disclosed are an expression vector comprising one or more
CC tumour necrosis factor inducible promoters and a recombinant host cell
CC transfected with one or more expression vectors. The TNF inducible
CC promoters, expression vectors and host cells are useful for identifying
CC promoters that are regulated by tumour necrosis factor or for identifying
CC candidate compounds for treating or preventing autoimmune disorders or
CC cancer. This sequence represents a tumour necrosis factor inducible
CC promoter of the invention.

XX SQ Sequence 771 BP; 186 A; 209 C; 253 G; 123 T; 0 U; 0 Other;
Query Match 100.0%; Score 140; DB 9; Length 771;
Best Local Similarity 100.0%; Pred. No. 6.7e-24;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGATCCGGAAGGCTCGCGTGTGTCGCTCAGACCGCGGAGGGGACG 60
DB 577 GGGTTCGGGAGGAGATCCGGAAGGCTCGCGTGTGTCGCTCAGACCGCGGAGGGGACG 636
QY 61 GGGCGGGGAGTAGTGGGGAGATGGAGACGAAGGGGAGGGAAGGACAGGGGAGGG 120
DB 637 GGGCGGGGAGTAGTGGGGAGATGGAGACGAAGGGGAGGGAAGGACAGGGGAGGG 696
QY 121 GAGGGTAAATAGTGGGCCAG 140
DB 697 GAGGGTAAATAGTGGGCCAG 716

RESULT 15
AAD41041
ID AAD41041 standard; DNA; 955 BP.
XX AAD41041;
XX 30-OCT-2002 (first entry)
XX Human 955-bp PCR product DNA.
XX Human; tumour necrosis factor; TNF; promoter; autoimmune disorder;
KW cancer; therapy; ds.
XX Homo sapiens.
XX Key
FH exon
FT 1. .443
FT /*tag= a
FT /note= Exon sequence of POLK contained in Hela 4.1
FT complement(1. .21)
FT /*tag= b
FT /bound_moiety= "Primer ON-GPBP-18m"
FT complement(443)
FT /*tag= c
FT /note= "Transcriptional start site"
FT 567. .735
FT /*tag= d
FT /note= Exon 1 of POLK
FT 726. .865
FT /*tag= e
FT /note= "140bp present in SpermPolk and SpermGPBP"
FT 851. .856
FT /*tag= f
FT 858. .955
FT /*tag= g
FT /note= "Part of exon 1 of COL4A3BP"
FT 858
FT /*tag= h
FT /note= "Transcriptional start site"
FT 930. .955
FT /*tag= i
FT /bound_moiety= "ON-GPBP-6c"
XX WO200246433-A2.
XX 13-JUN-2002.
XX 07-DEC-2001; 2001WO-EP014412.
XX 08-DEC-2000; 2000US-0254649P.
XX (SAUS/) SAUS J.
XX

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 20:07:37 ; Search time 106 Seconds
(without alignments)

2161.120 Million cell updates/sec

Title: US-10-008-721-6

Perfect score: 140

Sequence: 1 gggatcggggaggagatccc.....gagggttaaatagtggccag 140

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 8181359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA.*
- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
 - 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
 - 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
 - 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
 - 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	49	35.0	7218	1	US-08-232-463-14
C 2	44.6	31.9	101951	4	US-09-949-016-15648
C 3	44.4	31.7	46823	4	US-09-949-016-12723
C 4	44.4	31.7	46940	4	US-09-949-016-16252
C 5	44.4	31.7	99748	4	US-09-949-016-11990
C 6	44.4	31.7	99749	4	US-09-949-016-16518
C 7	44	31.4	500	4	US-09-866-108A-15742
C 8	43.8	31.3	601	4	US-09-949-016-135107
C 9	43.8	31.3	117807	4	US-09-949-016-15525
C 10	43.2	30.9	865	4	US-09-270-767-11042
C 11	43.2	30.9	16782	4	US-09-165-264-14
C 12	43	30.7	320	3	US-09-165-264-11
C 13	42.8	30.6	320	3	US-09-165-264-11
C 14	42.4	30.3	320	3	US-09-165-264-13
C 15	42.4	30.3	53526	3	US-08-658-136-2
C 16	42.4	30.3	53577	3	US-08-658-136-1
C 17	42.4	30.3	119032	4	US-09-949-016-12160
C 18	42.4	30.3	119032	4	US-09-949-016-17268
C 19	42.2	30.1	320	3	US-09-165-264-7
C 20	41.8	29.9	1469	4	US-09-865-879-12
C 21	41.6	29.7	318	3	US-09-165-264-12
C 22	41.2	29.4	319	3	US-09-165-264-8
C 23	41.2	29.4	264665	4	US-09-949-016-13747
C 24	41	29.3	253345	4	US-09-949-016-13639
C 25	41	29.3	253364	4	US-09-949-016-13639
C 26	40.6	29.0	936	4	US-09-270-767-4464
C 27	40.6	29.0	936	4	US-09-270-767-19746

C 28	40.6	29.0	9293	4	US-09-949-016-16801
C 29	40.6	29.0	37875	4	US-09-949-016-13182
C 30	40.4	28.9	204	4	US-09-107-433-2184
C 31	40.4	28.9	209	4	US-09-107-433-185
C 32	40.4	28.9	282	4	US-09-107-433-184
C 33	40.4	28.9	308	4	US-09-107-433-1723
C 34	40.4	28.9	612	4	US-09-107-433-1970
C 35	40.2	28.7	83617	4	US-09-949-016-12254
C 36	40.2	28.7	87870	4	US-09-949-016-14461
C 37	39.8	28.4	390890	4	US-09-949-016-14720
C 38	39.6	28.3	12001	1	US-08-458-568A-11
C 39	39.6	28.3	60950	4	US-09-949-016-14080
C 40	39.6	28.3	256287	4	US-09-949-016-14608
C 41	39.4	28.1	601	4	US-09-949-016-127819
C 42	39.4	28.1	601	4	US-09-949-016-127820
C 43	39.4	28.1	601	4	US-09-949-016-128156
C 44	39.4	28.1	601	4	US-09-949-016-128157
C 45	39.4	28.1	304533	4	US-09-949-016-15371

ALIGNMENTS

RESULT 1

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMWU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match 35.0% Score 49; DB 1; Length 7218;

RESULT 5
US-09-949-016-11990
; Sequence 11990, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11990
; LENGTH: 99748
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11990

Query Match 31.7%; Score 44.4; DB 4; Length 99748;
Best Local Similarity 61.0%; Pred. No. 0.015;
Matches 72; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 7 GGGAGGAGGATCCGGAAGGTCGCGTGTCTCAGACCGCGGGAGGGGAGCGGGCGG 66
Db 70064 GAGGAGGATAGAGAGAGGGGGGAGGAGAGCGAGAGGAGGGGAGAGAGG 70123

QY 67 GGAGTAGTGGGGAGAGTGGGAGCGAGCGAAGCGGGGAGGAAAGGACAGGGGAGGGAGG 124
Db 70124 AGAGCAAGGAGAGAGGGGGAGAGCGAGGAGCGAGGAGGAGGGGAGAGGAGG 70181

RESULT 6
US-09-949-016-16518
; Sequence 16518, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16518
; LENGTH: 99749
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16518

Query Match 31.7%; Score 44.4; DB 4; Length 99749;
Best Local Similarity 61.0%; Pred. No. 0.015;
Matches 72; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 7 GGGAGGAGGATCCGGAAGGTCGCGTGTCTCAGACCGCGGGAGGGGAGCGGGCGG 66
Db 70064 GAGGAGGATAGAGAGCGGGGAGGAGAGCGGAGGAGGAGGGGAGAGGAGG 70123

QY 67 GGAGTAGTGGGGAGAGTGGGAGCGAGCGAAGCGGGGAGGAAAGGACAGGGGAGGGAGG 124

Db 70124 AGAGCAAGGAGGAGAGCGGGGAGGAGGAGCGGAGGAGGAGGAGGAGGAGG 70181

RESULT 7
US-09-866-108A-15742/c
; Sequence 15742, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 15742
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-15742

Query Match 31.4%; Score 44; DB 4; Length 500;
Best Local Similarity 59.7%; Pred. No. 0.009;
Matches 74; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGGATCCGGAAGGTCGCGTGTCTCAGACCGCGGGAGGGGACG 60
Db 137 GGGGAGGGGAGGAAAGGTGGGAGGGGAGGGAGGTGGGAGGGGAGGTGGGAGGG 78

QY 61 GGGCGGGGAGTGTAGTGGGGGAGAAATGGGAGGACCAAGGGGAGGGGAAAGGACAGGGGAGGG 120
Db 77 AGGGGAGGGAGGTGGGAGGGGAGGGGAGGGGAGGAGCGGAGGGGAGGGAGGG 18

QY 121 GAGG 124
Db 17 GAGG 14

RESULT 8
US-09-949-016-135107/c
; Sequence 135107, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 135107
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-135107

Query Match      31.3%; Score 43.8; DB 4; Length 601;
Best Local Similarity 60.5%; Pred. No. 0.01;
Matches 72; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 7 GGGAGGAGGATCCGAAAGCTCGCGTGTGCGTCAGACCCGGAGGGGAGACGGGGCGG 66
Db 470 GAGAGGGAGAGGAGAGAGGATAGCGCAGAGGGAGAGGATCGGAGAGGAGAGAGGAGG 411
QY 67 GGAGTAGTGTGGGGAGAGATGGAGACGACGAAGGGAGGGGAAAGACAGAGGGGAGGGAGGG 125
Db 410 GAAAGGACAGGAGGAGGAGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGGAGGG 352

RESULT 9
US-09-949-016-15525/c
/ Sequence 15525, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 15525
/ LENGTH: 117807
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-15525
```

```
Query Match      31.3%; Score 43.8; DB 4; Length 117807;
Best Local Similarity 60.5%; Pred. No. 0.021;
Matches 72; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 7 GGGAGGAGGATCCGAAAGCTCGCGTGTGCGTCAGACCCGGAGGGGAGACGGGGCGG 66
Db 54166 GACAGGGAGAGGGAGAGGATAGCGCAGAGGGAGAGGATGGGGAGAGGAGAGGAGAGG 54107
QY 67 GGAGTAGTGTGGGGAGAGATGGAGAGCAGAGGGAGGGGAAAGACAGAGGGGAGGGAGGG 125
Db 54106 GAAAGGACAGGAGGAGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGGAGGG 54048
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RESULT 10
US-09-270-767-11042/c
/ Sequence 11042, Application US/09270767
/ Patent No. 6703491
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference; 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11042
/ LENGTH: 865
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
/ FEATURE:
/ OTHER INFORMATION: n means any nucleotide
US-09-270-767-11042
```

```
Query Match      30.9%; Score 43.2; DB 4; Length 865;
Best Local Similarity 57.4%; Pred. No. 0.016;
Matches 78; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GGGTTTCGGAGGAGGATCCGAAAGCTCGCGTGTGCGTCAGACCCGGAGGGGACG 60
Db 276 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 217
QY 61 GGGCGGGGGAGTAGTGTGGGGAGAGATGGAGACCGAAGGGGAGGGGAAAGACAGAGGGAGGG 120
Db 216 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 157
QY 121 GAGGGTAAATAGTGGG 136
Db 156 GGGGGGGGGTGTGGG 141
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```
RESULT 11
US-09-949-016-17291
/ Sequence 17291, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17291
/ LENGTH: 16782
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-17291
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```
Query Match      30.9%; Score 43.2; DB 4; Length 16782;
Best Local Similarity 57.4%; Pred. No. 0.023;
Matches 78; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 GGGTTTCGGAGGAGGATCCGAAAGCTCGCGTGTGCGTCAGACCCGGAGGGGACG 60
Db 1220 GGGGAGGGTAGGGGGTGGGGGGTGGGAGGGTAGGGGGGTGGGAGGGTGGGGGGGTG 1279
QY 61 GGGCGGGGAGTAGTGTGGGGAGAGATGGAGACCGAAGGGGAGGGGAAAGACAGAGGGAGGG 120
Db 1280 GGGAGGGTAGGGGGTGGGGGGTGGGGGGTGGGAGAGTAGGGGGGTGGGAGAGTAGGGGGGTGGG 1339
QY 121 GAGGGTAAATAGTGGG 136
Db 1340 GAGAGTAGGGGGTGGG 1355
```



```

RESULT 12
US-09-165-264-14
; Sequence 14, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-14

Query Match      30.7%; Score 43; DB 3; Length 320;
Best Local Similarity 56.8%; Pred. No. 0.015;
Matches 79; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGAGGGGACG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 169 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 228

QY 61 GGGCGGGGAGTAGTGGGGGAGAAATGGAGACGAGCGGAGGGGAGAAAGGACAGGGGAGGG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 229 GGGCGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 288

QY 121 GAGCGTAAATAGTGGGCCA 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 289 GGGGGGGGGGGGGGGGGTGTGCCA 307

RESULT 13
US-09-165-264-11
; Sequence 11, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11

Query Match      30.6%; Score 42.8; DB 3; Length 320;
Best Local Similarity 57.5%; Pred. No. 0.017;
Matches 77; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGAGGGGACG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 236

QY 61 GGGCGGGGAGTAGTGGGGGAGAAATGGAGACGAGCGGAGGGGAGGAGAAAGGACAGGGGAGGG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 296

QY 121 GAGCGTAAATAGT 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 297 GGGGGCAGATTTTG 310

RESULT 14
US-09-165-264-13
; Sequence 13, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayagamoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-13

Query Match      30.3%; Score 42.4; DB 3; Length 320;
Best Local Similarity 56.4%; Pred. No. 0.022;
Matches 79; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGAGGGGACG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 172 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 231

QY 61 GGGCGGGGAGTAGTGGGGGAGAAATGGAGACGAGCGGAGGGGAGGAGAAAGGACAGGGGAGGG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 232 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 291

QY 121 GAGCGTAAATAGTGGGCCAG 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 292 GGGGGGGGGGACGTGGACGAG 311

RESULT 15
US-08-658-136-2/c
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845

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; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-658-136-2
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Query Match 30.3%; Score 42.4; DB 3; Length 53526;
Best Local Similarity 57.6%; Pred. No. 0.045;
Matches 76; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCCGGCGTGTCCGTCAGACGCCGGGAGGGGACG 60
Db 34341 GGGAGGGCTGGGGGGAAGAGGAAAGGCTAGGGGAGGGAGGGAGGGCTAG 34282

QY 61 GGGCGGGGAGTAGTGGGGGAGATGGAGACGAAAGGGAGGGGAAAGGACAGGGGAGGG 120
Db 34281 GCGAGGGGAGGAGGGGAGGGGCTAGGGGAGGAAAGGGGAGGGGAGGGGAGGAGTG 34222

QY 121 GAGGTAANTAG 132
Db 34221 GAGGGCACAGAG 34210
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Search completed: June 12, 2005, 21:19:35
Job time : 109 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 20:20:48 ; Search time 329 Seconds
(without alignments)

2637.898 Million cell updates/sec

Title: US-10-008-721-6

Perfect score: 140

Sequence: 1 ggggtcggaggaggatccc.....gagggttaaatagtggccag 140

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	140	14	US-10-010-920-6
2	140	100.0	140	14	US-10-010-920-7
3	140	100.0	140	14	US-10-008-721-6
4	140	100.0	140	14	US-10-008-721-7
5	140	100.0	771	14	US-10-010-920-4
6	140	100.0	771	14	US-10-010-920-5
7	140	100.0	771	14	US-10-008-721-4

c	8	140	100.0	771	14	US-10-008-721-5	Sequence 5, Appli
	9	140	100.0	955	14	US-10-010-920-3	Sequence 3, Appli
	10	140	100.0	955	14	US-10-008-721-3	Sequence 3, Appli
c	11	50.4	36.0	424	19	US-10-437-963-49515	Sequence 49515, A
	12	48	34.3	985	20	US-10-425-115-91623	Sequence 91623, A
	13	47.6	34.0	408	19	US-10-021-323-5007	Sequence 5007, Ap
	14	47	33.6	588	19	US-10-021-323-9377	Sequence 9377, Ap
c	15	46.6	33.3	406	19	US-10-021-323-14271	Sequence 14271, A
c	16	46.6	33.3	891	20	US-10-425-115-146045	Sequence 146045,
	17	46.6	33.3	20345	17	US-10-292-798-705	Sequence 705, App
c	18	46.4	33.1	675	20	US-10-425-115-45871	Sequence 45871, A
c	19	46.2	33.0	92219	19	US-10-322-281-805	Sequence 805, App
c	20	46	32.9	692	20	US-10-425-115-16028	Sequence 16028, A
	21	45.8	32.7	804	18	US-10-424-599-100535	Sequence 100535,
c	22	45.6	32.6	614	20	US-10-425-115-94057	Sequence 94057, A
	23	45.6	32.6	629	19	US-10-021-323-9375	Sequence 9375, Ap
c	24	45.2	32.3	673	20	US-10-425-115-11145	Sequence 11145, A
c	25	45.2	32.3	1065	9	US-09-804-682-33	Sequence 33, Appl
	26	45	32.1	263	19	US-10-021-323-16665	Sequence 16665, A
c	27	45	32.1	668	19	US-10-437-963-3757	Sequence 3757, Ap
c	28	45	32.1	766	20	US-10-425-115-82176	Sequence 82176, A
c	29	45	32.1	925	19	US-10-437-963-44536	Sequence 44536, A
	30	45	32.1	1211	20	US-10-425-115-93385	Sequence 93385, A
	31	45	32.1	1385	17	US-10-398-221-1379	Sequence 1379, Ap
	32	45	32.1	1385	17	US-10-398-221-2930	Sequence 2930, Ap
c	33	44.8	32.0	294	20	US-10-425-115-79029	Sequence 79029, A
	34	44.8	32.0	447	19	US-10-021-323-10481	Sequence 10481, A
c	35	44.8	32.0	492	18	US-10-424-599-59619	Sequence 59619, A
c	36	44.8	32.0	545	19	US-10-437-963-56258	Sequence 56258, A
c	37	44.8	32.0	580	18	US-10-424-599-2320	Sequence 2320, Ap
	38	44.8	32.0	636	20	US-10-425-115-168126	Sequence 168126,
c	39	44.8	32.0	1087	18	US-10-424-599-81404	Sequence 81404, A
	40	44.8	32.0	189817	19	US-10-741-601-5660	Sequence 5660, Ap
	41	44.8	32.0	189817	21	US-10-741-600-17685	Sequence 17685, A
	42	44.6	31.9	522	13	US-10-027-632-134954	Sequence 134954,
	43	44.6	31.9	522	13	US-10-027-632-134955	Sequence 134955,
	44	44.6	31.9	522	17	US-10-027-632-134954	Sequence 134954,
	45	44.6	31.9	522	17	US-10-027-632-134955	Sequence 134955,

ALIGNMENTS

RESULT 1
US-10-010-920-6
; Sequence 6, Application US/10010920
; Publication NO. US20030027165A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences
; FILE REFERENCE: 98, 723-E3
; CURRENT APPLICATION NUMBER: US/10/010,920
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-920-6

Query Match	100.0%;	Score	140;	DB	14;	Length	140;
Best Local Similarity	100.0%;	Pred. NO.	3.5e-29;				
Matches	140;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	GGGTTTCGGGAGGAGGATCCCGAAGGCTCGGCGTGTCCGTCAGACGCCGGGGGGGACG	60				
Db	1	GGGTTTCGGGAGGAGGATCCCGAAGGCTCGGCGTGTCCGTCAGACGCCGGGGGGGACG	60				
Qy	61	GGGCGGGGAGTAGTGTGGGGGAGATGGGAGGACGAAGGGGGGAGGACGACGGGGGGG	120				

Db 61 GGGCGGGAGTACTGGGGAGAAATGGGAGACGAAGGGAGGGGAAAGGACAGGGGAGGG 120
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QY 121 GAGGGTAAATAGTGGGCCAG 140
|
Db 121 GAGGGTAAATAGTGGGCCAG 140
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RESULT 2

US-10-010-920-7/c
; Sequence 7, Application US/10010920
; Publication No. US20030027165A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences
; FILE OF INVENTION: and methods for using
; FILE REFERENCE: 98,723-E3
; CURRENT APPLICATION NUMBER: US/10/010,920
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-920-7

Query Match 100.0%; Score 140; DB 14; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.5e-29;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGCTGTCGCGTCAGACGCCGGAGGGGAGCG 60
|
Db 140 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGCTGTCGCGTCAGACGCCGGAGGGGAGCG 81
|
QY 61 GGGCGGGGAGTACTGGGGAGAAATGGGAGACGAAGGGAGGGGAAAGGACAGGGGAGGG 120
|
Db 80 GGGCGGGGAGTACTGGGGAGAAATGGGAGACGAAGGGAGGGGAAAGGACAGGGGAGGG 21
|
QY 121 GAGGGTAAATAGTGGGCCAG 140
|
Db 20 GAGGGTAAATAGTGGGCCAG 1
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RESULT 3

US-10-008-721-6
; Sequence 6, Application US/10008721
; Publication No. US20030082745A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: TNF-Inducible Promoters and Methods for Using
; FILE REFERENCE: 98,723-E1
; CURRENT APPLICATION NUMBER: US/10/008,721
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-008-721-6

Query Match 100.0%; Score 140; DB 14; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.5e-29;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGCTGTCGCGTCAGACGCCGGAGGGGAGCG 60
|
Db 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGCTGTCGCGTCAGACGCCGGAGGGGAGCG 60
|

QY 61 GGGCGGGAGTACTGGGGAGAAATGGGAGACGAAGGGAGGGGAAAGGACAGGGGAGGG 120
|
Db 61 GGGCGGGGAGTACTGGGGAGAAATGGGAGACGAAGGGAGGGGAAAGGACAGGGGAGGG 120
|
QY 121 GAGGGTAAATAGTGGGCCAG 140
|
Db 121 GAGGGTAAATAGTGGGCCAG 140
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RESULT 4

US-10-008-721-7/c
; Sequence 7, Application US/10008721
; Publication No. US20030082745A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: TNF-Inducible Promoters and Methods for Using
; FILE REFERENCE: 98,723-E1
; CURRENT APPLICATION NUMBER: US/10/008,721
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-008-721-7

Query Match 100.0%; Score 140; DB 14; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.5e-29;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGCTGTCGCGTCAGACGCCGGAGGGGAGCG 60
|
Db 140 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGCTGTCGCGTCAGACGCCGGAGGGGAGCG 81
|
QY 61 GGGCGGGGAGTACTGGGGAGAAATGGGAGACGAAGGGAGGGGAAAGGACAGGGGAGGG 120
|
Db 80 GGGCGGGGAGTACTGGGGAGAAATGGGAGACGAAGGGAGGGGAAAGGACAGGGGAGGG 21
|
QY 121 GAGGGTAAATAGTGGGCCAG 140
|
Db 20 GAGGGTAAATAGTGGGCCAG 1
|

RESULT 5

US-10-010-920-4
; Sequence 4, Application US/10010920
; Publication No. US20030027165A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences
; FILE REFERENCE: 98,723-E3
; CURRENT APPLICATION NUMBER: US/10/010,920
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-920-4

Query Match 100.0%; Score 140; DB 14; Length 771;
Best Local Similarity 100.0%; Pred. No. 2.6e-29;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGCTGTCGCGTCAGACGCCGGAGGGGAGCG 60
|

Db 577 GGGTTCCGGAGGAGATCCCGAAGGCTCGCGTGTCCGTCAGACGCCGGAGGGGACG 636
 Qy 61 GGGCGGGAGTGTAGTGGGGGAGATGGGAGGACGAAGGGGAGGGAAGGACAGGGGAGGG 120
 Db 637 GGGCGGGAGTGTAGTGGGGGAGATGGGAGGACGAAGGGGAGGGAAGGACAGGGGAGGG 696
 Qy 121 GAGGGTAAATAGTGGGCCAG 140
 Db 697 GAGGGTAAATAGTGGGCCAG 716

RESULT 6
 US-10-010-920-5/c
 ; Sequence 5, Application US/10010920
 ; Publication No. US20030027165A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saus, Juan
 ; TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences
 ; FILE REFERENCE: 98,723-E3
 ; CURRENT APPLICATION NUMBER: US/10/010,920
 ; PRIOR FILING DATE: 2001-12-07
 ; PRIOR APPLICATION NUMBER: 60/254,649
 ; PRIOR FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-010-920-5

Query Match 100.0%; Score 140; DB 14; Length 771;
 Best Local Similarity 100.0%; Pred. No. 2.6e-29;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGGTTCCGGAGGAGATCCCGAAGGCTCGCGTGTCCGTCAGACGCCGGAGGGGACG 60
 Db 195 GGGTTCCGGAGGAGATCCCGAAGGCTCGCGTGTCCGTCAGACGCCGGAGGGGACG 136
 Qy 61 GGGCGGGAGTGTAGTGGGGGAGATGGGAGGACGAAGGGGAGGGAAGGACAGGGGAGGG 120
 Db 135 GGGCGGGAGTGTAGTGGGGGAGATGGGAGGACGAAGGGGAGGGAAGGACAGGGGAGGG 76
 Qy 121 GAGGGTAAATAGTGGGCCAG 140
 Db 75 GAGGGTAAATAGTGGGCCAG 56

RESULT 7
 US-10-008-721-4
 ; Sequence 4, Application US/10008721
 ; Publication No. US20030082745A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saus, Juan
 ; TITLE OF INVENTION: TNF-Inducible Promoters and Methods for Using
 ; FILE REFERENCE: 98,723-E1
 ; CURRENT APPLICATION NUMBER: US/10/008,721
 ; PRIOR FILING DATE: 2001-12-07
 ; PRIOR APPLICATION NUMBER: 60/254,649
 ; PRIOR FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-008-721-4

Query Match 100.0%; Score 140; DB 14; Length 771;
 Best Local Similarity 100.0%; Pred. No. 2.6e-29;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTTCCGGAGGAGATCCCGAAGGCTCGCGTGTCCGTCAGACGCCGGAGGGGACG 60
 Db 577 GGGTTCCGGAGGAGATCCCGAAGGCTCGCGTGTCCGTCAGACGCCGGAGGGGACG 636
 Qy 61 GGGCGGGAGTGTAGTGGGGGAGATGGGAGGACGAAGGGGAGGGAAGGACAGGGGAGGG 120
 Db 637 GGGCGGGAGTGTAGTGGGGGAGATGGGAGGACGAAGGGGAGGGAAGGACAGGGGAGGG 696
 Qy 121 GAGGGTAAATAGTGGGCCAG 140
 Db 697 GAGGGTAAATAGTGGGCCAG 716

RESULT 8
 US-10-008-721-5/c
 ; Sequence 5, Application US/10008721
 ; Publication No. US20030082745A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saus, Juan
 ; TITLE OF INVENTION: TNF-Inducible Promoters and Methods for Using
 ; FILE REFERENCE: 98,723-E1
 ; CURRENT APPLICATION NUMBER: US/10/008,721
 ; CURRENT FILING DATE: 2001-12-07
 ; PRIOR APPLICATION NUMBER: 60/254,649
 ; PRIOR FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-008-721-5

Query Match 100.0%; Score 140; DB 14; Length 771;
 Best Local Similarity 100.0%; Pred. No. 2.6e-29;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGGTTCCGGAGGAGATCCCGAAGGCTCGCGTGTCCGTCAGACGCCGGAGGGGACG 60
 Db 195 GGGTTCCGGAGGAGATCCCGAAGGCTCGCGTGTCCGTCAGACGCCGGAGGGGACG 136
 Qy 61 GGGCGGGAGTGTAGTGGGGGAGATGGGAGGACGAAGGGGAGGGAAGGACAGGGGAGGG 120
 Db 135 GGGCGGGAGTGTAGTGGGGGAGATGGGAGGACGAAGGGGAGGGAAGGACAGGGGAGGG 76
 Qy 121 GAGGGTAAATAGTGGGCCAG 140
 Db 75 GAGGGTAAATAGTGGGCCAG 56

RESULT 9
 US-10-010-920-3
 ; Sequence 3, Application US/10010920
 ; Publication No. US20030027165A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saus, Juan
 ; TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences
 ; FILE REFERENCE: 98,723-E3
 ; CURRENT APPLICATION NUMBER: US/10/010,920
 ; CURRENT FILING DATE: 2001-12-07
 ; PRIOR APPLICATION NUMBER: 60/254,649
 ; PRIOR FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 955
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-010-920-3

Query Match 100.0%; Score 140; DB 14; Length 955;

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Best Local Similarity 100.0%; Pred. No. 2.5e-29;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGATCCCGAAGGCTCGCGCTGTTCGCTCAGACGCCGGAGGGGAGCG 60
Db 726 GGGTTCGGGAGGAGATCCCGAAGGCTCGCGCTGTTCGCTCAGACGCCGGAGGGGAGCG 785

QY 61 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGACAGGGGAGGG 120
Db 786 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGACAGGGGAGGG 845

QY 121 GAGGGTAAATAGTGGGCCAG 140
Db 846 GAGGGTAAATAGTGGGCCAG 865

RESULT 10
US-10-008-721-3
; Sequence 3, Application US/10008721
; Publication No. US20030082745A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: TNF-Inducible Promoters and Methods for Using
; FILE REFERENCE: 98,723-E1
; CURRENT APPLICATION NUMBER: US/10/008,721
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-008-721-3

Query Match 100.0%; Score 140; DB 14; Length 955;
Best Local Similarity 100.0%; Pred. No. 2.5e-29;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGATCCCGAAGGCTCGCGCTGTTCGCTCAGACGCCGGAGGGGAGCG 60
Db 726 GGGTTCGGGAGGAGATCCCGAAGGCTCGCGCTGTTCGCTCAGACGCCGGAGGGGAGCG 785

QY 61 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGACAGGGGAGGG 120
Db 786 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGACAGGGGAGGG 845

QY 121 GAGGGTAAATAGTGGGCCAG 140
Db 846 GAGGGTAAATAGTGGGCCAG 865

RESULT 11
US-10-437-963-49515/c
; Sequence 49515, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 49515
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; LENGTH: 424
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52092C.1
US-10-437-963-49515

Query Match 36.0%; Score 50.4; DB 19; Length 424;
Best Local Similarity 60.0%; Pred. No. 9.1e-05;
Matches 84; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGATCCCGAAGGCTCGCGCTGTTCGCTCAGACGCCGGAGGGGAGCG 60
Db 270 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGACAGGGGAGGG 211

QY 61 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGACAGGGGAGGG 120
Db 210 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGAGAGGGGGGGGG 151

QY 121 GAGGGTAAATAGTGGGCCAG 140
Db 150 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGAGAGGGGGGGGG 151

RESULT 12
US-10-425-115-91623
; Sequence 91623, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 91623
; LENGTH: 985
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(985)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_183557C.1
US-10-425-115-91623

Query Match 34.3%; Score 48; DB 20; Length 985;
Best Local Similarity 59.6%; Pred. No. 0.00035;
Matches 81; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 GGGTTCGGGAGGAGATCCCGAAGGCTCGCGCTGTTCGCTCAGACGCCGGAGGGGAGCG 60
Db 536 GGGTTCGGGAGGAGATCCCGAAGGCTCGCGCTGTTCGCTCAGACGCCGGAGGGGAGCG 595

QY 61 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGACAGGGGAGGG 120
Db 596 GGGCGGGGAGTACTGGGGAGAGATCGGAGCAGCAAGGGGAGGGGAAAGGACAGGGGAGGG 655

QY 121 GAGGGTAAATAGTGGGG 136
Db 656 GGGGGTGGGTTCGGGG 671

RESULT 13
US-10-021-323-5007
; Sequence 5007, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021.323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 5007
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3826-001-Q1-N6-H3
US-10-021-323-5007

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Query Match      34.0%; Score 47.6; DB 19; Length 408;
Best Local Similarity 69.1%; Pred. No. 0.00053;
Matches 65; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 43 GAGCCCGGAGGAGCGCGCGGGAGTAGTGGGGGAGAGTGGGAGGACGAGGAGG 102
Db 142 GAAGAGGGGGGGCAAGAGGGGGGGGGGAGGAGGGGGGGGAGGAGCGGAGG 201

Qy 103 GGAAGGACAGGGGAGGGGAGGGTAAATAGTGGG 136
Db 202 GGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 235

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RESULT 14
US-10-021-323-9377
; Sequence 9377, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021.323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 9377
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(588)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3828-025-Q6-K6-D5
US-10-021-323-9377

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Query Match      33.6%; Score 47; DB 19; Length 588;
Best Local Similarity 62.2%; Pred. No. 0.00073;
Matches 74; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 7 GGGAGGAGGATCCCGAGGCTCGCGGTCTCAGACGCCCGGAGGAGGAGCGGGCGG 66
Db 397 GGGAGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 456

Qy 67 GGAGTAGTGGGGAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 125
Db 457 GAGGGGGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 515

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RESULT 15
US-10-021-323-14271/c
; Sequence 14271, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021.323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 14271
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(406)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3829-031-Q6-N6-H2
US-10-021-323-14271

Query Match      33.3%; Score 46.6; DB 19; Length 406;
Best Local Similarity 60.8%; Pred. No. 0.001;
Matches 76; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGGTCTCGCTCAGACGCCCGGAGGAGGAGCG 60
Db 321 GGGGGGGGGGGAGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 262

Qy 61 GGGCGGGGAGTAGTGGGGGAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db 261 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 202

Qy 121 GAGGG 125
Db 201 GGGGG 197

Search completed: June 12, 2005, 21:25:09
Job time : 331 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 19:55:18 ; Search time 1736 Seconds
(without alignments)

3069.699 Million cell updates/sec

Title: US-10-008-721-6

Perfect score: 140

Sequence: 1 ggggtcggaggaggatccc.....gagggtaaatagtgggcccag 140

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	52.9	697	4	BI826689 603077454
2	73.6	52.6	506	6	CB446475 700183 MA
3	73.6	52.6	624	6	CB446113 697902 MA
4	60.4	43.1	293	5	BA472815 DKEZD686D
5	57.6	41.1	536	4	BI831357 603074343
6	56.6	40.4	999	9	CL464985 SAIL1231
7	54.4	38.9	299	9	CR163087 Reverse s
8	54.4	38.9	854	9	AG521132 Mus muscu
9	54.4	38.9	1391	2	BA451555 HVSMEH009
10	53.4	38.1	800	9	AG553158 Mus muscu
11	53.2	38.0	1102	9	CL463500 SAIL1187
12	52.4	37.4	872	5	BX385509 BX385509
13	52	37.1	887	8	A2192949 SP_1022 B
14	52	37.1	951	4	BI958037 HVSMEH001
15	52	37.1	1036	9	AG419622 Mus muscu
16	51.8	37.0	830	9	CNS028FQ
17	51.8	37.0	898	9	AG381174 Mus muscu
18	51.6	36.9	1024	8	CC275787 CH261-133
19	51.4	36.7	744	9	AG490609 Mus muscu
20	51.4	36.7	866	9	AG520508 Mus muscu
21	51.2	36.6	743	2	BP631446 HVSMEB001
22	51.2	36.6	949	9	AG326267 Mus muscu
23	51.2	36.6	1072	7	CV520572 0089P0047
24	51.2	36.6	1229	8	CC319720 TAM32-14E

25	51.2	36.6	1560	9	CL081488	CH216-162
26	51.2	36.6	1686	8	CC189908	CH261-611
27	51.2	36.6	1971	8	CC207340	CH261-181
28	51	36.4	567	9	AG462381	Mus muscu
29	51	36.4	1031	9	AG324949	Mus muscu
30	51	36.4	1072	9	CL462217	SAIL115
31	50.8	36.3	425	7	CK089660	C024F74.3
32	50.8	36.3	773	8	BZ050814	jnf64all.
33	50.8	36.3	909	9	CL462489	SAIL1166
34	50.6	36.1	876	9	AG395251	Mus muscu
35	50.6	36.1	904	9	AG049068	Pan trogl
36	50.6	36.1	933	9	CNS006XG	AL066047 Drosophil
37	50.6	36.1	1201	9	CNS016F9	AL106671 Drosophil
38	50.4	36.0	591	9	AG124266	AG124266 Pan trogl
39	50.4	36.0	668	9	AG139415	AG139415 Pan trogl
40	50.4	36.0	713	8	BH944647	BH944647 obu77C09.
41	50.4	36.0	723	9	AG123920	AG123920 Pan trogl
42	50.4	36.0	770	9	AG038994	Pan trogl
43	50.4	36.0	998	9	AG388659	Mus muscu
44	50.4	36.0	1305	8	BZ694620	SP_Ba004
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ALIGNMENTS

BI826689 697 bp mRNA linear EST 04-OCT-2001
LOCUS 603077454F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5169180 5',
DEFINITION mRNA sequence.

ACCESSION BI826689

VERSION BI826689.1 GI:15938239

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 697)

NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-x@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM11420 row: 1 column: 13

High quality sequence stop: 686.

FEATURES Location/Qualifiers

1..697

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5169180"

/tissue_type="medulla"

/lab_host="DH10B"

/clone_lib="NIH_MGC_119"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site: 1: NotI;

Site 2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH_MGC Library."

ORIGIN

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Query Match      52.9%; Score 74; DB 4; Length 697;
Best Local Similarity 98.8%; Pred. No. 1.4e-06;
Matches 85; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 55 GGGACGGGGCGGGAGTAGTGGGGAGAAATGGGAGGACGAAGGGAGGGGAAAGGACAGG 114
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Db 1 GGGACGGGGCGGGAGTAGTGGGGAGAAATGGGAGGACGAAGGGAGGGGAAAGGACA-G 59

QY 115 GGGAGGGAGGGTAATAGTGGGCCAG 140
    |||
Db 60 GGGAGGGAGGGTAATAGTGGGCCAG 85

RESULT 2
LOCUS CB446475 506 bp mRNA linear EST 26-MAR-2003
DEFINITION 700183 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION CB446475
VERSION CB446475.1 GI:29252857
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 506)
AUTHORS Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329
Plate: FOY8054 row: K column: 21
Seq primer: TAGAAGGCACAGTCGAGG.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/notes="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

FEATURES
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Best Local Similarity 81.6%; Pred. No. 1.7e-06;
Matches 111; Conservative 0; Mismatches 19; Indels 6; Gaps 2;

QY 5 TCGGGAGGAGGATCCCGAAGGCTCGGCGTTCGCGTCAGACGCCGGAGGGGACCGGGC 64
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Db 359 TTGCGGAGGGAACCTCCGAGCCTCGGCGTTCGCGTCAGACGTTGGAGGGGGACCGGGC 418

QY 65 GGGAGTAGTGGGGAGAAATGGGAGGACGAAGGGAGGAAAGGACAGGGGAGGGAGG 124
    |||
Db 419 GGGGAGCAG-AGGGGAGAAATGGGAGGACGAAGGGAGG-----GAAGAGGGGAGGGAGG 472

QY 125 GTAAATAGTGGGCCAG 140
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Db 473 GTAAATAGTGGGCTAG 488

RESULT 3
LOCUS CB446475 506 bp mRNA linear EST 26-MAR-2003
DEFINITION 700183 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION CB446475
VERSION CB446475.1 GI:29252857
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 506)
AUTHORS Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329
Plate: FOY8054 row: K column: 21
Seq primer: TAGAAGGCACAGTCGAGG.
Location/Qualifiers
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/mol_type="mRNA"
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/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/notes="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

FEATURES
source
Query Match 52.6%; Score 73.6; DB 6; Length 506;
Best Local Similarity 81.6%; Pred. No. 1.7e-06;
Matches 111; Conservative 0; Mismatches 19; Indels 6; Gaps 2;

QY 5 TCGGGAGGAGGATCCCGAAGGCTCGGCGTTCGCGTCAGACGCCGGAGGGGACCGGGC 64
    |||
Db 359 TTGCGGAGGGAACCTCCGAGCCTCGGCGTTCGCGTCAGACGTTGGAGGGGGACCGGGC 418

QY 65 GGGAGTAGTGGGGAGAAATGGGAGGACGAAGGGAGGAAAGGACAGGGGAGGGAGG 124
    |||
Db 419 GGGGAGCAG-AGGGGAGAAATGGGAGGACGAAGGGAGG-----GAAGAGGGGAGGGAGG 472

QY 125 GTAAATAGTGGGCCAG 140
    |||
Db 473 GTAAATAGTGGGCTAG 488

RESULT 4
LOCUS CB472815 293 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686D23150.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 293)
AUTHORS Bloecker,H., Boecker,M., Mewes,H.W., Weil,B., Amlid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.

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CB446113/c
LOCUS CB446113 624 bp mRNA linear EST 26-MAR-2003
DEFINITION 697902 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB446113
VERSION CB446113.1 GI:29252495
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 624)
AUTHORS Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329
Plate: FOY8054 row: K column: 21
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
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/clone_lib="MARC 6BOV"
/notes="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN
Query Match 52.6%; Score 73.6; DB 6; Length 624;
Best Local Similarity 81.6%; Pred. No. 1.7e-06;
Matches 111; Conservative 0; Mismatches 19; Indels 6; Gaps 2;

QY 5 TCGGGAGGAGGATCCCGAAGGCTCGGCGTTCGCGTCAGACGCCGGAGGGGACCGGGC 64
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Db 348 TTGCGGAGGGAACCTCCGAGCCTCGGCGTTCGCGTCAGACGTTGGAGGGGGACCGGGC 289

QY 65 GGGAGTAGTGGGGAGAAATGGGAGGACGAAGGGAGGAAAGGACAGGGGAGGGAGG 124
    |||
Db 288 GGGGAGCAG-AGGGGAGAAATGGGAGGACGAAGGGAGG-----GAAGAGGGGAGGGAGG 235

QY 125 GTAAATAGTGGGCCAG 140
    |||
Db 234 GTAAATAGTGGGCTAG 219

RESULT 4
LOCUS BX472815/c 293 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686D23150.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 293)
AUTHORS Bloecker,H., Boecker,M., Mewes,H.W., Weil,B., Amlid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.

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Class:   Image
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                    modified TAIL-PCR strategy"

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MODIFIED TATU-FCK Strategy:

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Query Match      40.4%; Score 56.6; DB 9; Length 999;
Best Local Similarity 63.2%; Pred. No. 0.0089;
Matches 86; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGAGGGGACG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 730 GGGGGGGGAGGGGGCGCGCGAGAGNAGGCGAGTAGTCCGCAAGCGCGGGGAGGGGG 671

QY 61 GGGCGGGGAGTAGTGGGGGAGGAATGGGAGACGAAGGGGAGGGAAGGACAGCGGAGGG 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 670 GGGGGGGGAGGGGGCGCGGGGGGAGGGGGGGCGCAGGGGGGGGGGGGAGGGGGCGAGGG 611

QY 121 GAGGGTAAATAGTGGG 136
Db 610 GGGGGGGAGGGGGGGG 595

RESULT 7
LOCUS      CR163087      299 bp      DNA      linear      GSS 06-JUL-2004
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and
             chromosome engineering clone MHPPI87p04, genomic survey sequence.
ACCESSION  CR163087
VERSION    GI:49941936
KEYWORDS   GSS: genome survey sequence; MICER.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 299)
AUTHORS    Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J., and Bradley,A.
TITLE      Direct Submission
JOURNAL    Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES   Location/Qualifiers
            source          1..299
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:10090"
                        /clone="MHPPI87p04"
                        /clone_lib="MHP"

ORIGIN
Query Match      38.9%; Score 54.4; DB 9; Length 299;
Best Local Similarity 62.5%; Pred. No. 0.029;
Matches 85; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGAGGGGACG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 110 GGGGGGAGAGGGGAGGGGGGAGGGGGGGGGGGGGGGGGGGGGGAGGAGGGGGGGGGG 169

QY 61 GGGCGGGGAGTAGTGGGGGAGGAATGGGAGACGAAGGGGAGGGAAGGACAGCGGAGGG 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 170 GGGGGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGAGGAGGGAAGGAGGGGGGAGGG 229

QY 121 GAGGGTAAATAGTGGG 136
Db 230 GGGGGGAAGGGGGGGG 245

RESULT 8
AGS21132/c
LOCUS      AGS21132      854 bp      DNA      linear      GSS 04-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-428B08.TJ, genomic survey
             sequence.
ACCESSION  AGS21132
VERSION    GI:48228545
KEYWORDS   GSS.
SOURCE     Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
REFERENCE  2 (bases 1 to 854)
AUTHORS    Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@sc.riken.jp. URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
            Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institute, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector      : pBACe3.6
R.Site 1    : EcoRI
R.Site 2    : EcoRI
FEATURES   Location/Qualifiers
            source          1..854
                        /organism="Mus musculus molossinus"
                        /mol_type="genomic DNA"
                        /sub_species="molossinus"
                        /db_xref="taxon:57486"
                        /clone="MSMg01-428B08.TJ"
                        /sex="male"
                        /tissue_type="mixture of kidney and spleen"
                        /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match      38.9%; Score 54.4; DB 9; Length 854;
Best Local Similarity 62.5%; Pred. No. 0.027;
Matches 85; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCCGGAGGAGGATCCCGAAGGCTCGCGTGTCTCGCTCAGACGCCGGGAGGGGACG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 525 GGGCGCGGGGAGGAGGGGGGGGGGGGGGGGGGGGGGAGAGAGAGAGGGGGGGGGGAGG 466

QY 61 GGGCGGGGAGTAGTGGGGGAGGAATGGGAGACGAAGGGGAGGGGAAAGGACAGCGGAGGG 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 465 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 406

QY 121 GAGGGTAAATAGTGGG 136
Db 405 GGGGGGAGAGGGGGAGG 390

RESULT 9
BE455155
LOCUS      BE455155      1391 bp      mRNA      linear      EST 22-OCT-2001
DEFINITION HVSMEH0096G10f Hordeum vulgare 5-45 DAP spike EST library
            HVCNDA0009 (5 to 45 DAP) Hordeum vulgare subsp. vulgare cDNA clone
            HVSMEH0096G10f, mRNA sequence.
ACCESSION  BE455155
VERSION    BE455155.2 GI:16322260
KEYWORDS   EST.
SOURCE     Hordeum vulgare subsp. vulgare
            Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Hordeum.
            1 (bases 1 to 1391)
REFERENCE  1 (bases 1 to 1391)
AUTHORS    Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
            Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
            Fenton,R.D., Close,S.J., Oates,R. and Main,D.

```

TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library

JOURNAL Unpublished (2001)

COMMENT On Jul 26, 2000 this sequence version replaced gi:9464547.

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 164
Seq primer: AATTAAACCTCACTAAAGGG
High quality sequence start: 248
High quality sequence stop: 1317.

FEATURES

source

1..1391

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Morex"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="HVSMEH0096G10f"

/tissue_type="5-45 DAP Spike"

/lab_host="SOLR"

/clone_lib="Hordeum vulgare 5-45 DAP spike EST library HVCNA0009 (5 to 45 DAP)"

/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI; plants were grown in the greenhouse at the University of California, Riverside (Penton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Penton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi) in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

ORIGIN

Query Match 38.9%; Score 54.4; DB 2; Length 1391;
Best Local Similarity 62.5%; Pred. No. 0.027;
Matches 85; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGAGGAGGATCCCGAAGGCTCGCGGTCTCGCGTCAGACGCCGGAGGGGACG 60
DB 817 GGG 876

QY 61 GGGGGGGGGAGTGTAGTGGGGGAGAAATGGGAGGACGAAGGGGGGGAAGGACAGGGGAGGG 120
DB 877 GGGGGGGGGAGAGGG 936

QY 121 GAGGGTAAATAGTGGG 136
DB 937 TTGGGAATGGGTGG 952

RESULT 10
AG553158/c

LOCUS AG553158 800 bp DNA linear GSS 05-JUN-2004

DEFINITION Mus musculus molossinus DNA, clone:MSMg01-470B03.T7, genomic survey sequence.

ACCESSION AG553158

VERSION AG553158.1 GI:48313849

KEYWORDS GSS.

SOURCE Mus musculus molossinus

ORGANISM Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Hattori M., Toyoda A., Noguchi H., Kojima T. and Sakaki Y.
BAC end Sequences of Library MSMg01

AUTHORS Hattori M., Toyoda A., Noguchi H., Kojima T. and Sakaki Y.

TITLE Direct Submission

JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan 1-7-22 Suehiro-chou, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: <http://hgp.gsc.riken.go.jp/>, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Teukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS

Sequencing : T7

LIBRARY Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

FEATURES

source

1..800

/organism="Mus musculus molossinus"

/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMg01-470B03.T7"

/sex="male"

/tissue_type="mixture of kidney and spleen"

/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 38.1%; Score 53.4; DB 9; Length 800;
Best Local Similarity 62.2%; Pred. No. 0.046;
Matches 84; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGAGGAGGATCCCGAAGGCTCGCGGTCTCGCGTCAGACGCCGGAGGGGACG 60
DB 712 GGGGGCTGTAGGGGGAGGGGGGGGGGAGGGGGGGAGGGAGGGGGGAGAAGGGAG 653

QY 61 GGGCGGGGGAGTGTAGTGGGGGAGAAATGGGAGGACGAAGGGGGGAGGAGGAGGGGAGGG 120
DB 652 GGGGGGGGGGGGGGGGGTGGGAGGGGGGGGGAGGGGGGGGGGGGGGGGGGGGGGG 593

QY 121 GAGGGTAAATAGTGG 135
DB 592 GAGGGGGTATAGGG 578

RESULT 11
CL463500

LOCUS CL463500 1102 bp DNA linear GSS 31-MAR-2004

DEFINITION SAIL1187 All.v1 SAIL Collection Arabidopsis thaliana genomic clone

ACCESSION SAIL_1187_All.v1, genomic survey sequence.

VERSION CL463500.1 GI:45866405

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)


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/tissue_type="Rachis"
/lab_host="TUC121"
/clone_lib="Hordeum vulgare rachis EST library HVCDA0015
(normal)"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Plants were grown at Washington State University, and
Pullman, WA in a greenhouse, the rachises were excised, and
frozen in liquid nitrogen (Kleinhofs lab). In the TU Close
lab at the University of California, Riverside total RNA
was prepared, poly(A) was purified, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Chin). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
sequence has been trimmed to remove vector sequence and
contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)."

ORIGIN

Query Match          37.1%; Score 52; DB 4; Length 951;
Best Local Similarity 63.7%; Pred. No. 0.092;
Matches 79; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY      1   CGGTTCGGAGGAGGATCCGAAGGCTCGCGTGTCGCAGACGCCGGAGGGGACG 60
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       542 GGCGGGGGGGGAGGAGCGGAGGGGGGGCGGTGCGCGGGCGGGGGGGCGG 601

QY      . 61   GCGCGCGGAGTAGTGTGGGCGAGAATCGGAGCGACGAAGGGGAGGAAAGCACGGGAGGG 120
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       602 GGCGGTGGGGGGGAGGGGAGCGGGGGGGCGAGGGAGGGGGGGGGGGGGGGGG 661

QY      121 GAGG 124
        ||| |||
Db       662 GAGG 665


RESULT 15
AG419622 LOCUS
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-290E22.T7, genomic survey
sequence.
ACCESSION AG419622
VERSION AG419622.1 GI:48062685
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1036)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgpc.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center.
```

